

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: December 6, 2002, 22:09:46 : Search time 230 Seconds  
(without alignments)  
14931.728 Million cell updates/sec

Title: US-10-025-514-15

Perfect score: 1525

Sequence: 1 tctagaccatgagacaccc.....ccagtcaggccttagtcgac 1525

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_101002.\*  
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2: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.\*  
3: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.\*  
4: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.\*  
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23: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.\*  
24: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1525	100.0	1525	24	ABK88025 DNA sequence encod
2	1197.4	78.5	1582	24	ABK88027 DNA sequence encod
3	1197.4	78.5	1756	24	ABK88026 DNA sequence encod
4	1191.6	78.1	1525	24	ABK88022 DNA sequence encod
5	1188.8	78.0	1756	24	ABK88023 DNA sequence encod
6	1187	77.8	1582	24	ABK88024 DNA sequence encod
7	1182	77.5	1182	24	ABK88015 DNA encoding human
8	628.4	41.2	1260	19	AAV41730 Codon-optimised RA
9	432.2	28.3	1312	16	AA089254 Human alpha-1-trypt

10	432.2	28.3	1312	19	AAV28471	Nucleotide sequenc
11	432.2	28.3	1312	21	AA290199	Human alpha-1-anti
12	429.2	28.1	1367	22	AA945052	cDNA encoding nove
13	429	28.1	1185	19	AAV41726	Native coding sequ
14	429	28.1	1352	13	AAQ31403	Human alpha-1 anti
15	429	28.1	1352	24	ABU67511	Thyroid cancer rel
16	429	28.1	1371	24	ABK84495	Human cDNA differe
17	429	28.1	1371	24	ABL67510	Thyroid cancer rel
18	429	28.1	1433	10	AA91077	Sequence encoding
19	429	28.1	1434	5	AA40078	Sequence encoding
20	429	28.1	1434	20	AA83548	Human alpha-1-anti
21	429	28.1	5932	21	AA245928	Nucleotide sequenc
22	429	28.1	6142	21	AA245932	Nucleotide sequenc
23	429	28.1	6142	21	AA245933	Nucleotide sequenc
24	429	28.1	6565	21	AA245925	Nucleotide sequenc
25	429	28.1	6714	21	AA245930	Nucleotide sequenc
26	429	28.1	6924	21	AA245934	Nucleotide sequenc
27	429	28.1	6924	21	AA245935	Nucleotide sequenc
28	429	28.1	6981	21	AA245931	Nucleotide sequenc
29	429	28.1	7054	21	AA245927	Nucleotide sequenc
30	428.6	28.1	7405	21	AA245926	Nucleotide sequenc
31	427.6	28.0	1189	13	AAQ21125	Alpha-1-antitrypsi
32	427.4	28.0	1352	18	AA72858	Human alpha-1-anti
33	425.8	27.9	1312	10	AA97127	Sequence of alpha-
34	425.8	27.9	1434	10	AA90341	Sequence of alpha-
35	425.4	27.9	1185	7	AA60417	Human alpha 1-anti
36	424.2	27.8	1378	13	AAQ23746	Alpha-1 antitrypsi
37	424.2	27.8	1396	11	AAQ03184	Entire sequence of
38	422.6	27.7	1423	6	AA50425	Sequence encoding
39	421	27.6	1259	6	AA50540	Sequence of human
40	421	27.6	1378	6	AA50021	Sequence encoding
41	407	26.7	1390	22	AA23089	Osteoarthritis tis
42	402.6	26.4	2013	24	ABL59152	Sequence of fusion
43	372.6	24.4	1242	18	AA79493	Protease inhibitor
44	359.8	23.6	1242	18	AA78180	Recombinant squirr
45	357	23.4	1312	10	AA91078	Alpha-1-antitrypsi

#### ALIGNMENTS

RESULT 1  
ABK88025  
ID ABK88025 standard; DNA; 1525 BP.  
XX  
AC ABK88025;  
XX  
DT 07-OCT-2002 (first entry)  
XX  
DE DNA sequence encoding rSLAP1 fusion protein.  
XX  
KW rSLAP1; gene; ds; Alzheimer's disease; tumour angiogenesis;  
KW malaria; emphysema; asthma; chronic obstructive pulmonary disease;  
KW cystic fibrosis; otitis media; otitis externa; HIV; psoriasis; eczema;  
KW human immunodeficiency virus; atopic dermatitis; muscular dystrophy;  
KW herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease;  
KW tumour metastasis; osteoporosis; Paget's disease; scleroderma;  
KW glomerulonephritis; hypertension.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT RBS 6..8  
FT /tag= a  
FT /standard\_name= "Ribosome binding site"  
FT CDS 9..1520  
FT /tag= b  
FT /product= "rSLAP1 fusion protein"  
FT FT DNA sequence encod  
FT misc\_feature 12..1193  
FT /tag= c  
FT /note= "AAT coding region"  
FT misc\_feature 1194..1196

Mon Dec 9 12:50:32 2002

FT /tag= d  
 FT /note= "linking codon"  
 FT 1197..1517  
 FT /tag= e  
 FT /note= "SLPI coding region"

WO200250287-A2.

27-JUN-2002.

18-DEC-2001; 2001WO-US49256.

18-DEC-2000; 2000US-256699P.

20-NOV-2001; 2001US-331966P.

(ARRI-) ARRIVA PHARM INC.

Barr PJ, Gibson HL, Pemberton P;

WPI; 2002-500631/53.

P-PSDB; AAU99884.

Novel fusion protein useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, comprises a first protease inhibitor comprising alpha 1-antitrypsin and a second protease inhibitor -

Example 3; Page 89-90; 134pp; English.

This invention relates to a novel fusion protein comprising a first protease inhibitor comprising an alpha1-antitrypsin or its functionally active portion and a second protease inhibitor or its functionally active portion. The fusion proteins of the invention may act as an inhibitor of protease activity. The fusion protein of the invention is useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, chronic obstructive pulmonary disease, cystic fibrosis, otitis media, otitis externa or HIV infection, or for treating an individual suffering from or at risk for a disease or disorder involving unwanted protease activity. The proteins are useful for treating dermatological diseases such as atopic dermatitis, eczema and psoriasis, in inflammatory responses to viral infection, and for treating herpes infection, corneal or epidermal ulceration, chronic non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease, tumour metastasis and tumour angiogenesis, gastric ulceration, osteoporosis, Paget's disease, glomerulonephritis, scleroderma, malaria, bacterial infection, Alzheimer's disease, hypertension and muscular dystrophy. The present sequence represents the DNA encoding the rSLAP1 fusion protein of the invention.

Sequence 1525 BP; 467 A; 287 C; 314 G; 457 T; 0 other;

Query Match 100.0%; Score 1525; DB 24; Length 1525;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 TCTAGACCATGGAAGACCTCAAGCGGCGCGCTCAAAAAACCGACACGATCATCAG 60  
 QY 61 ACCAAGACCATCGGACTTTTAAATAAATTACTCCAAATTTAGCCGAATTTGCTTTTCTT 120  
 Db 61 ACCAAGACCATCGGACTTTTAAATAAATTACTCCAAATTTAGCCGAATTTGCTTTTCTT 120  
 QY 121 TGTATAGCAATTTAGCTCATCAAGTAATTTCTACTAACATTTTTTTTAGTCTCTGTTCTA 180  
 Db 121 TGTATAGCAATTTAGCTCATCAAGTAATTTCTACTAACATTTTTTTTAGTCTCTGTTCTA 180  
 QY 181 TTGCCACTGCTTTCGCCATGTTGAGTTTAGGTACTAAAGCCGATACCATGACGAGATTT 240  
 Db 181 TTGCCACTGCTTTCGCCATGTTGAGTTTAGGTACTAAAGCCGATACCATGACGAGATTT 240  
 QY 241 TAGAAGGTTTAACTTTAATTTGACCGAATCCACGAAGCCCAAAATTCACGAGGGTTTTC 300  
 Db 241 TAGAAGGTTTAACTTTAATTTGACCGAATCCACGAAGCCCAAAATTCACGAGGGTTTTC 300

Db 241 TAGAAGGTTTAACTTTAATTTGACCGAATCCACGAAGCCCAAAATTCACGAGGGTTTTC 300  
 QY 301 AAGAGTTGTTGAGAACTTTGAATCAACCTGATCTCAATTTGCAATTAACCTACTGGTAACG 360  
 Db 301 AAGAGTTGTTGAGAACTTTGAATCAACCTGATCTCAATTTGCAATTAACCTACTGGTAACG 360  
 QY 361 GTTTATTTTCTGCTGAAGGTTTAAAAATTTGGTTGACAAATTTCTTAGAAGCGTCAAGAAAC 420  
 Db 361 GTTTATTTTCTGCTGAAGGTTTAAAAATTTGGTTGACAAATTTCTTAGAAGCGTCAAGAAAC 420  
 QY 421 TATATCATAGTGAGGCTTTTACCCTTAATTTTGGTGATCTGAGGAAGCTAAAAAGCAA 480  
 Db 421 TATATCATAGTGAGGCTTTTACCCTTAATTTTGGTGATCTGAGGAAGCTAAAAAGCAA 480  
 QY 481 TTAATGATTTGTTGAGAAAGCGCACCGGTAAGATGTTGACCTAGCTTAAAGAAATTAG 540  
 Db 481 TTAATGATTTGTTGAGAAAGCGCACCGGTAAGATGTTGACCTAGCTTAAAGAAATTAG 540  
 QY 541 ATCGTGATACCGCTTTCGCACTAGTTAACTATATTTTTTCAAGGGTAAGTGGGAACGTC 600  
 Db 541 ATCGTGATACCGCTTTCGCACTAGTTAACTATATTTTTTCAAGGGTAAGTGGGAACGTC 600  
 QY 601 CTTTCGAGGTTTAAAGTACTGAAGAGGAGATTTTCATGTTGATCAAGTACTACTGTCGA 660  
 Db 601 CTTTCGAGGTTTAAAGTACTGAAGAGGAGATTTTCATGTTGATCAAGTACTACTGTCGA 660  
 QY 661 AAGTTCCAATGATGAAGAGCTGGGTATGTTCAATATTAACATTTCAACATTTGCAAAAAATTAAGTT 720  
 Db 661 AAGTTCCAATGATGAAGAGCTGGGTATGTTCAATATTAACATTTGCAAAAAATTAAGTT 720  
 QY 721 CTTGGGCTTTAATTAAGTAAGTATTTAGGTAACGCTACTGCTATTTTTTTTACCAGAGC 780  
 Db 721 CTTGGGCTTTAATTAAGTAAGTATTTAGGTAACGCTACTGCTATTTTTTTTACCAGAGC 780  
 QY 781 AAGGTAAGCTTCAACATTTAGAGATGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGA 840  
 Db 781 AAGGTAAGCTTCAACATTTAGAGATGAGTGAATGAGTGAATGAGTGAATGAGTGAATGAGTGA 840  
 QY 841 AGAACGAGGATCTGCTGAGCGCTTCTGCACCTGCGCAAGTTAAGTATCAACGGTACTTT 900  
 Db 841 AGAACGAGGATCTGCTGAGCGCTTCTGCACCTGCGCAAGTTAAGTATCAACGGTACTTT 900  
 QY 901 ACGACTTAAATCTGTTTATAGGCGAGTATAGTATTAACAAAGTTTTTTTCTAACGGTGGCG 960  
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 QY 961 ATTTGAGTGGTGTACTGAAGAGCTCCCAATTAATTAAGTGAAGCTGTTTCAACAAAGCGG 1020  
 Db 961 ATTTGAGTGGTGTACTGAAGAGCTCCCAATTAATTAAGTGAAGCTGTTTCAACAAAGCGG 1020  
 QY 1021 TCTTAACCTATTGATGAAGAGGTTACCGAGCGCGCGCTATGTTCTCTGGAAGCTATTTC 1080  
 Db 1021 TCTTAACCTATTGATGAAGAGGTTACCGAGCGCGCGCTATGTTCTCTGGAAGCTATTTC 1080  
 QY 1081 CAATGAGCATTTCCACAGAGTATTAATTAATTAACCAATTCGTTTCTCATGATCGAGC 1140  
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 QY 1141 AGAACACTAAAGCCCATTTGTTTATGAGTGAAGTGTGTAACCCCAACCTCAGAAGATGTCG 1200  
 Db 1141 AGAACACTAAAGCCCATTTGTTTATGAGTGAAGTGTGTAACCCCAACCTCAGAAGATGTCG 1200  
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 Db 1201 GAAAGTCTTTTCAAGCGCGGTTGTTTGTCCACAAAGAGTCCGCTCAATGTTTGAGATACA 1260  
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QY 721 CTGGGCTTATTAATGAAGTATTAGTAAACGCTACTGCTATTTTTTTTACCAGACG 780
Db 721 CTGGGCTTATTAATGAAGTATTAGTAAACGCTACTGCTATTTTTTTTACCAGACG 780
QY 781 AAGGTAAGCTTCAACATTTAGAGAAATGAGTTGACTCATGACATTTACTAAATTTTAG 840
Db 781 AAGGTAAGCTTCAACATTTAGAGAAATGAGTTGACTCATGACATTTACTAAATTTTAG 840
QY 841 AGAAGGAGGATCGTGTAGCCCTTCTCTGACCTGCGCAAAAGTTAAGTATCACCGGTACTT 900
Db 841 AGAAGGAGGATCGTGTAGCCCTTCTCTGACCTGCGCAAAAGTTAAGTATCACCGGTACTT 900
QY 901 ACGACTTAAATCTGTTTTAGCCAGTTAGTATTAACAAAGTTTTTCTAACGGTCCG 960
Db 901 ACGACTTAAATCTGTTTTAGCCAGTTAGTATTAACAAAGTTTTTCTAACGGTCCG 960
QY 961 ATTTCAGTGGTGTACTGAAGAAGCTCCATTAATAATTGAGTAAAGCTGTTTACAAAAGCCG 1020
Db 961 ATTTCAGTGGTGTACTGAAGAAGCTCCATTAATAATTGAGTAAAGCTGTTTACAAAAGCCG 1020
QY 1021 TCTTAACATTTGATGAAAGGTTACCGAGCGCGCGCTATGTTCTCTGGAAGCTATTC 1080
Db 1021 TCTTAACATTTGATGAAAGGTTACCGAGCGCGCGCTATGTTCTCTGGAAGCTATTC 1080
QY 1081 CAATGAGCATTCACCCAGAGTAAATTAATAAACCATTCGTTTTTCTGATGATCAGC 1140
Db 1081 CAATGAGCATTCACCCAGAGTAAATTAATAAACCATTCGTTTTTCTGATGATCAGC 1140
QY 1141 AGAACACTAAAGGCCATTGTTATGGTAAAGTTGTCAACCCCACTCAGAAAGATGCC 1199
Db 1141 AGAACACTAAAGGCCATTGTTATGGTAAAGTTGTCAACCCCACTCAGAAAGATGCC 1199

RESULT 3
ID ABR88026
XX ABR88026 standard; DNA; 1756 BP.
AC ABR88026;
XX
XX 07-OCT-2002 (first entry)
XX
XX DNA sequence encoding rTAP1 fusion protein.
DE
DE rTAP1; gene; ds; Alzheimer's disease; tumour angiogenesis;
KW malaria; emphysema; asthma; chronic obstructive pulmonary disease;
KW cystic fibrosis; otitis media; otitis externa; HIV; psoriasis; eczema;
KW human immunodeficiency virus; atopic dermatitis; muscular dystrophy;
KW herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease;
KW tumour metastasis; osteoporosis; Paget's disease; scleroderma;
KW glomerulonephritis; hypertension.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT RBS 6..8
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FT /standard_name= "Ribosome binding site"
FT CDS 9..1751
FT /tag= b
FT /product= "rTAP1 fusion protein"
FT misc_feature 12..1193
FT /tag= c
FT /note= "AAT coding region"
FT misc_feature 1194..1196
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FT /note= "linking codon"
FT misc_feature 1197..1748
FT /tag= e
FT /note= "TIMP-1 coding region"
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XX WO200250287-A2.
XX 27-JUN-2002.
XX 18-DEC-2001; 2001WO-US49256.
XX 18-DEC-2000; 2000US-256699P.
XX 20-NOV-2001; 2001US-331966P.
XX (ARRI-) ARRIVA PHARM INC.
XX Barr PJ, Gibson HL, Pemberton P;
XX WPI; 2002-500631/53.
XX P-PSDB; AAU99889.
XX Novel fusion protein useful for inhibiting protease activity associated
XX with a disorder such as emphysema, asthma, comprises a first protease
XX inhibitor comprising alpha 1-antitrypsin and a second protease
XX inhibitor -
XX Example 3; Page 92-93; 134pp; English.
XX This invention relates to a novel fusion protein comprising a first
XX protease inhibitor comprising an alpha 1-antitrypsin or its functionally
XX active portion and a second protease inhibitor or its functionally
XX active portion. The fusion proteins of the invention may act as an
XX inhibitor of protease activity. The fusion protein of the invention
XX is useful for inhibiting protease activity associated with a disorder
XX such as emphysema, asthma, chronic obstructive pulmonary disease,
XX cystic fibrosis, otitis media, otitis externa or HIV infection, or
XX for treating an individual suffering from or at risk for a disease or
XX disorder involving unwanted protease activity. The proteins are useful
XX for treating dermatological diseases such as atopic dermatitis, eczema
XX and psoriasis, in inflammatory responses to viral infection, and for
XX treating herpes infection, corneal or epidermal ulceration, chronic
XX non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease,
XX tumour metastasis and tumour angiogenesis, gastric ulceration,
XX osteoporosis, Paget's disease, glomerulonephritis, scleroderma, malaria,
XX bacterial infection, Alzheimer's disease, hypertension and muscular
XX dystrophy. The present sequence represents the DNA encoding the
XX rTAP1 fusion protein of the invention.
XX
XX Sequence 1756 BP; 493 A; 394 C; 374 G; 495 T; 0 other;
XX
Query Match 78.5%; Score 1197.4; DB 24; Length 1756;
Best Local Similarity 99.9%; Pred. No. 5.7e-291;
Matches 1198; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 1 TCTAGACCATGGAAGACCCCTCAAGCGGACGCCGCTCAAAAACCCGACCATCATCAGC 60
QY 61 ACCAAGACCATCGACTTTTAAATAAATACTCCAAATTTAGCCGAATTTGCTTTTCTT 120
Db 61 ACCAAGACCATCGACTTTTAAATAAATACTCCAAATTTAGCCGAATTTGCTTTTCTT 120
QY 121 TGTATAGACAATTAGCTCATCAAAAGTAATTTCTACTAACATTTTTTTTAGTCCTGTTCTA 180
Db 121 TGTATAGACAATTAGCTCATCAAAAGTAATTTCTACTAACATTTTTTTTAGTCCTGTTCTA 180
QY 181 TTGCCACTGCTTTCGCCATGTTGAGTTTAGGTACTAAAGCCGATACCCATGAGGATTT 240
Db 181 TTGCCACTGCTTTCGCCATGTTGAGTTTAGGTACTAAAGCCGATACCCATGAGGATTT 240
QY 241 TAGAAGGTTTTAACTTTAATTTGACCGAAATCCAGAACCCCAAAATTCAGAGGGTTTC 300
Db 241 TAGAAGGTTTTAACTTTAATTTGACCGAAATCCAGAACCCCAAAATTCAGAGGGTTTC 300
QY 301 AAGAGTTGTTGAGAACCTTTGAATCAACCTGATTCCTCAATTTGCAATTAACCTGGTAAAC 360
Db 301 AAGAGTTGTTGAGAACCTTTGAATCAACCTGATTCCTCAATTTGCAATTAACCTGGTAAAC 360
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QY 361 GTTATTATTTCTGAAGGTTTAAATTCGTTGACAAATTCCTAGAGACGTCACAGAAC 420
DB 361 GTTATTATTTCTGAAGGTTTAAATTCGTTGACAAATTCCTAGAGACGTCACAGAAC 420
QY 421 TATATCATAGTGAAGGCTTTTACCGTTTAAATTTGGTGATACACTAGGAGCTAAAGAGCAAA 480
DB 421 TATATCATAGTGAAGGCTTTTACCGTTTAAATTTGGTGATACACTAGGAGCTAAAGAGCAAA 480
QY 481 TTAATGATTATGTTGAGAAAGGACCCAGGGTAAAGATCGTTGACCTAGTAAAGAAATTAG 540
DB 481 TTAATGATTATGTTGAGAAAGGACCCAGGGTAAAGATCGTTGACCTAGTAAAGAAATTAG 540
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DB 541 ATCGTGATACCGCTTCGCACTAGTTAACTATATTTTTTCAAGGCTAAGTGGAGACGTC 600
QY 601 CTTTCGAGGTTAAAGATACCTGAAGAGGAAGATTTTCATGTTGATCAAGTACTACTGTCA 660
DB 601 CTTTCGAGGTTAAAGATACCTGAAGAGGAAGATTTTCATGTTGATCAAGTACTACTGTCA 660
QY 661 AAGTTCCATGATGAAGAGACTGGGTATGTTCAATATTCATATTCGCAAAATTAAGTT 720
DB 661 AAGTTCCATGATGAAGAGACTGGGTATGTTCAATATTCATATTCGCAAAATTAAGTT 720
QY 721 CTTGGGCTTATTAAATGAAGTATTTAGGTAACGCTACTGCTATTTTTTTTACACGAGC 780
DB 721 CTTGGGCTTATTAAATGAAGTATTTAGGTAACGCTACTGCTATTTTTTTTACACGAGC 780
QY 781 AAGTTAAGCTTCAACATTTAGAGAAATGAGTTGACTCATGACATTAATTAATTTTAG 840
DB 781 AAGTTAAGCTTCAACATTTAGAGAAATGAGTTGACTCATGACATTAATTAATTTTAG 840
QY 841 AGAACGAGGATCGTCTAGCGCTTCTGCACTGCAAGTAAAGTTAAGTATCAACGGTACTT 900
DB 841 AGAACGAGGATCGTCTAGCGCTTCTGCACTGCAAGTAAAGTTAAGTATCAACGGTACTT 900
QY 901 ACACGTTAAATCTGTTTAAAGGCTTAAAGTATTAACCAAGTTTCTTAACGGTGCGC 960
DB 901 ACACGTTAAATCTGTTTAAAGGCTTAAAGTATTAACCAAGTTTCTTAACGGTGCGC 960
QY 961 ATTTGAGTGGTGTACTGAAGAGCTCCATTTAAATTTAGTAAAGCTGTTCAAGAGCG 1020
DB 961 ATTTGAGTGGTGTACTGAAGAGCTCCATTTAAATTTAGTAAAGCTGTTCAAGAGCG 1020
QY 1021 TCCTTAATGATGATGAAGGTTACGAGGCGCGCGCGCTATGTTCTCGAAGCTATTTC 1080
DB 1021 TCCTTAATGATGATGAAGGTTACGAGGCGCGCGCGCTATGTTCTCGAAGCTATTTC 1080
QY 1081 CAATGAGCATTCACCAAGGTTAAATTTAAATAAACCATTCGTTTCTGTGATGATGAGC 1140
DB 1081 CAATGAGCATTCACCAAGGTTAAATTTAAATAAACCATTCGTTTCTGTGATGATGAGC 1140
QY 1141 AGAAGCTAAAGAGGCTGTTTATGGGTAAGGTTGTCACCACTCAGAGATGTC 1199
DB 1141 AGAAGCTAAAGAGGCTGTTTATGGGTAAGGTTGTCACCACTCAGAGATGTC 1199

RESULT 4
ABK8022
ID ABK8022 standard; DNA; 1525 BP.
XX
AC ABK8022;
XX
DT 07-OCT-2002 (first entry)
XX
DE DNA sequence encoding SLAP1 fusion protein.
XX
KW Yeast; alpha factor; gene; ds; Alzheimer's disease; SLAP1;
KW malaria; emphysema; asthma; chronic obstructive pulmonary disease;
KW cystic fibrosis; otitis media; otitis externa; HIV; psoriasis; eczema;
KW human immunodeficiency virus; atopic dermatitis; muscular dystrophy;
KW herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease;
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KW tumour metastasis; tumour angiogenesis; osteoporosis; Paget's disease;  
glomerulonephritis; scleroderma; hypertension.

OS Homo sapiens.  
OS Synthetic.

Key Location/Qualifiers  
RBS 6..8

FT /\*tag= a  
/standard\_name= "Ribosome binding site"  
9..1520

FT /\*tag= b  
/product= "SLAP1 fusion protein"

FT misc\_feature 12..332  
/\*tag= c  
/note= "SLPI coding region"

FT misc\_feature 333-335  
/\*tag= d

FT /\*tag= "linking codon"

FT misc\_feature 336..1517  
/\*tag= e  
/note= "AAT coding region"

PN WO200250287-A2.

XX 27-JUN-2002.

XX 18-DEC-2001; 2001WO-US49256.

XX 18-DEC-2000; 2000US-256699P.

XX 20-NOV-2001; 2001US-331966P.

XX (ARRI-) ARRIVA PHARM INC.

XX Barr PJ, Gibson HL, Pemberton P;

XX WPI; 2002-500631/53.

XX P-PSDB; ANU99881.

XX Novel fusion protein useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, comprises a first protease inhibitor comprising alpha 1-antitrypsin and a second protease inhibitor -

XX Example 1; Page 73-73; 134pp; English.

XX This invention relates to a novel fusion protein comprising a first protease inhibitor comprising an alpha1-antitrypsin or its functionally active portion and a second protease inhibitor or its functionally active protein. The fusion proteins of the invention may act as an inhibitor of protease activity. The fusion protein of the invention is useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, chronic obstructive pulmonary disease, cystic fibrosis, otitis media, otitis externa or HIV infection, or for treating an individual suffering from or at risk for a disease or disorder involving unwanted protease activity. The proteins are useful for treating dermatological diseases such as atopic dermatitis, eczema and psoriasis, in inflammatory responses to viral infection, and for treating herpes infection, corneal or epidermal ulceration, chronic non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease, tumour metastasis and tumour angiogenesis, gastric ulceration, osteoporosis, Paget's disease, glomerulonephritis, scleroderma, malaria, bacterial infection, Alzheimer's disease, hypertension and muscular dystrophy. The present sequence represents the DNA encoding the SLAP1 fusion protein of the invention.

XX Sequence 1525 BP; 467 A; 286 C; 314 G; 458 T; 0 other;

Query Match 78.1%; Score 1191.6; DB 24; Length 1525;  
Best Local Similarity 99.7%; Pred. No. 1.6e-289;  
Matches 1194; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCTAGACCATGGAAGACCTCAAGGCGAGCGCGCTCAAAAAACCGACCATCATCAGC 60



CC is useful for inhibiting protease activity associated with a disorder  
CC such as emphysema, asthma, chronic obstructive pulmonary disease,  
CC cystic fibrosis, otitis media, otitis external or HIV infection, or  
CC for treating an individual suffering from or at risk for a disease or  
CC disorder involving unwanted protease activity. The proteins are useful  
CC for treating dermatological diseases such as atopic dermatitis, eczema  
CC and psoriasis, in inflammatory responses to viral infection, and for  
CC treating herpes infection, corneal or epidermal ulceration, chronic  
CC non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease,  
CC tumour metastasis and tumour angiogenesis, gastric ulceration,  
CC osteoporosis, Paget's disease, glomerulonephritis, scleroderma, malaria,  
CC bacterial infection, Alzheimer's disease, hypertension and muscular  
CC dystrophy. The present sequence represents the DNA encoding the  
CC TAP1 fusion protein of the invention.  
XX  
SQ

Sequence 1756 BP; 493 A; 395 C; 373 G; 495 T; 0 other;

Query Match 78.0%; Score 1188.8; DB 24; Length 1756;  
Best Local Similarity 99.8%; Pred. No. 8.3e-289;  
Matches 1190; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 CCATGGAAGACCCCTCAAGCGGCGCTCAAAAACCCACACAGTCATCAGACCAAG 56  
DB 562 CCATGGAAGACCCCTCAAGCGGCGCTCAAAAACCCACACAGTCATCAGACCAAG 621  
QY 67 ACCATCCGACTTTTAATAAAATTTACTCCAAATTTAGCCGAATTTGCTTTTCTTGATA 126  
DB 622 ACCATCCGACTTTTAATAAAATTTACTCCAAATTTAGCCGAATTTGCTTTTCTTGATA 581  
QY 127 GACAATAGTCATCAAAAGTAATCTACTTAACATTTTTTTTATAGTCCTGTTCTATTGCCA 186  
DB 682 GACAATAGTCATCAAAAGTAATCTACTTAACATTTTTTTTATAGTCCTGTTCTATTGCCA 741  
QY 187 CTGCTTTCCGCTGTTGAGTTTGTAGTACTTAAAGCCGATACCCATGACGAGATTTAGAA 246  
DB 742 CTGCTTTCCGCTGTTGAGTTTGTAGTACTTAAAGCCGATACCCATGACGAGATTTAGAA 801  
QY 247 GTTTAAACCTTTAATTTGACCGAATCCCAAGAGCCCAATTTACGAGGCTTTTCAAGAGT 306  
DB 802 GTTTAAACCTTTAATTTGACCGAATCCCAAGAGCCCAATTTACGAGGCTTTTCAAGAGT 861  
QY 307 TGTGAGAACTTTGAATCAACCTGATCTCAATTTGCAATTTAACTACTGTAACGGTTTAT 366  
DB 862 TGTGAGAACTTTGAATCAACCTGATCTCAATTTGCAATTTAACTACTGTAACGGTTTAT 921  
QY 367 TTTTGTCTGAAGCTTTAAATTTGGTTGACAAATTTCTAGAACGCTCAAGAACTATATC 426  
DB 922 TTTTGTCTGAAGCTTTAAATTTGGTTGACAAATTTCTAGAACGCTCAAGAACTATATC 981  
QY 427 ATAGTGAGGCTTTTACCGTTAATTTTGGTGATCTAGGAGCTTAAAGCAAAATTAATG 486  
DB 982 ATAGTGAGGCTTTTACCGTTAATTTTGGTGATCTAGGAGCTTAAAGCAAAATTAATG 1041  
QY 487 ATTATGTTGAGAAAGCCACCCAGGTAAGATCGTTGACCTAGTTTAAAGAAATTTAGATCGTG 546  
DB 1042 ATTATGTTGAGAAAGCCACCCAGGTAAGATCGTTGACCTAGTTTAAAGAAATTTAGATCGTG 1101  
QY 547 ATACCGCTCTTCGACCTAGTTTAACTATATTTTTCAGGGTAAGTGGGAACGCTCTTCG 606  
DB 1102 ATACCGCTCTTCGACCTAGTTTAACTATATTTTTCAGGGTAAGTGGGAACGCTCTTCG 1161  
QY 607 AGTTTAAAGATCTGAAGAGGAAGATTTTCATGTTGATCAAGTTTACTGTCAAAGTTC 666  
DB 1162 AGTTTAAAGATCTGAAGAGGAAGATTTTCATGTTGATCAAGTTTACTGTCAAAGTTC 1221  
QY 667 CAATGATGAAAAGACTGGGTATGTTCAATTAATTCATTTGCAAAATTAAGTCTTGGG 726  
DB 1222 CAATGATGAAAAGACTGGGTATGTTCAATTAATTCATTTGCAAAATTAAGTCTTGGG 1281  
QY 727 TCTTATTATGAATGATTTAGTAAAGCTACTGCTATTTTTTTTTTACCAGACGAAGTA 786  
DB 1282 TCTTATTATGAATGATTTAGTAAAGCTACTGCTATTTTTTTTTTACCAGACGAAGTA 1341

QY 787 AGCTTCAACATTTAGAGAAATGAGTTGACTCATGACATTTACTATAATTTTAGAGAACG 846  
DB 1342 AGCTTCAACATTTAGAGAAATGAGTTGACTCATGACATTTACTATAATTTTAGAGAACG 1401  
QY 847 AGGATCGTGTAGCGCTTCTCTGACACCTGCGCAAGTTAAAGTATCACCGGTACTTACGACT 906  
DB 1402 AGGATCGTGTAGCGCTTCTCTGACACCTGCGCAAGTTAAAGTATCACCGGTACTTACGACT 1461  
QY 907 TAAATCTGTTTATAGGCGAGTTAGGTATTAACAAAGTTTTTCTTAAACGGTCCGATTTGA 966  
DB 1462 TAAATCTGTTTATAGGCGAGTTAGGTATTAACAAAGTTTTTCTTAAACGGTCCGATTTGA 1521  
QY 967 GTGGTGTTACTCAAGAACCTCCATTAATAATGAGTAAAGCTGTTACAAAGCCGCTCTAA 1026  
DB 1522 GTGGTGTTACTCAAGAACCTCCATTAATAATGAGTAAAGCTGTTACAAAGCCGCTCTAA 1581  
QY 1027 CTATTGATGAAAGGGTACCAGCGCGCGCGCTATGTTCTCGAAGCTATTCCAATGA 1086  
DB 1582 CTATTGATGAAAGGGTACCAGCGCGCGCGCTATGTTCTCGAAGCTATTCCAATGA 1641  
QY 1087 GCATTCACACAGAGTTAAATTTAATAAACCATTCGTTTTTCTGATGATCGAGCAGAACA 1146  
DB 1642 GCATTCACACAGAGTTAAATTTAATAAACCATTCGTTTTTCTGATGATCGAGCAGAACA 1701  
QY 1147 CTAAAGGCCCATTTGTTATGGTAAAGTTGTCAACCCCAACTCAGAAGATGTC 1198  
DB 1702 CTAAAGGCCCATTTGTTATGGTAAAGTTGTCAACCCCAACTCAGAAGATGTC 1753  
RESULT 6  
ABK88024  
ID ABR88024 standard; DNA; 1582 BP.  
XX  
AC ABR88024;  
XX  
DT 07-OCT-2002 (first entry)  
XX  
DE DNA sequence encoding N-TAP1 fusion protein.  
XX  
KW N-TAP1; gene; ds; Alzheimer's disease; tumour angiogenesis;  
KW malaria; emphysema; asthma; chronic obstructive pulmonary disease;  
KW cystic fibrosis; otitis media; otitis externa; HIV; psoriasis; eczema;  
KW human immunodeficiency virus; atopic dermatitis; muscular dystrophy;  
KW herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease;  
KW tumour metastasis; osteoporosis; Paget's disease; scleroderma;  
KW glomerulonephritis; hypertension.  
OS Homo sapiens.  
OS Synthetic.  
XX  
Key Location/Qualifiers  
RBS 6..8  
FT /\*tag= a  
FT /standard\_name= "Ribosome binding site"  
FT 9..1577  
FT /\*tag= b  
FT /product= "N-TAP1 fusion protein"  
FT 12..389  
FT /\*tag= c  
FT /note= "TIMP-1 coding region"  
FT 390..392  
FT /\*tag= d  
FT /note= "linking codon"  
FT 393..1574  
FT /\*tag= e  
FT /note= "AAT coding region"  
PN WO2002050287-A2.  
XX  
PD 27-JUN-2002.  
XX  
PF 18-DEC-2001; 2001WO-US49256.  
XX





FT /\*tag= a  
FT /product= "Alpha-1-antitrypsin"  
FT /partial  
FT /note= "No start or stop codon shown"  
XX  
PN WO200250287-A2.  
XX  
XX  
PD 27-JUN-2002.  
XX  
XX 18-DEC-2001; 2001WO-US49256.  
XX  
XX 18-DEC-2000; 2000US-256699P.  
PR 20-NOV-2001; 2001US-331966P.  
XX  
XX (ARRI-) ARRIVA PHARM INC.  
PA  
XX  
XX Barr PJ, Gibson HL, Pemberton P;  
XX  
XX WPI; 2002-500631/53.  
DR P-PSDB; AAU99873.  
XX  
XX

Novel fusion protein useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, comprises a first protease inhibitor comprising alpha 1-antitrypsin and a second protease inhibitor -

Disclosure; Page 24-25; 134pp; English.

XX This invention relates to a novel fusion protein comprising a first  
XX protease inhibitor comprising an alpha1-antitrypsin or its functionally  
XX active portion and a second protease inhibitor or its functionally  
XX active protein. The fusion proteins of the invention may act as an  
XX inhibitor of protease activity. The fusion protein of the invention  
XX is useful for inhibiting protease activity associated with a disorder  
XX such as emphysema, asthma, chronic obstructive pulmonary disease,  
XX cystic fibrosis, otitis media, otitis external or HIV infection, or  
XX for treating an individual suffering from or at risk for a disease or  
XX disorder involving unwanted protease activity. The proteins are useful  
XX for treating dermatological diseases such as atopic dermatitis, eczema  
XX and psoriasis, in inflammatory responses to viral infection, and for  
XX treating herpes infection, corneal or epidermal ulceration, chronic  
XX non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease,  
XX tumour metastasis and tumour angiogenesis, gastric ulceration,  
XX osteoporosis, Paget's disease, glomerulonephritis, scleroderma,  
XX bacterial infection, Alzheimer's disease, hypertension and muscular  
XX dystrophy. The present sequence represents the DNA encoding the human  
XX alpha-1-antitrypsin (AAT) protein used to create the fusion protein  
XX of the invention.

SQ Sequence 1182 BP; 369 A; 214 C; 229 G; 370 T; 0 other;

Query Match 77.5%; Score 1182; DB 24; Length 1182;  
Best Local Similarity 100.0%; Pred. No. 3.7e-287;  
Matches 1182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GAAGACCCCTCAAGCGCAGCGCGCTCAAAAACCGACACCATCATCAGCACCAGACCAT 71  
DB 1 GAAGACCCCTCAAGCGCAGCGCGCTCAAAAACCGACACCATCATCAGCACCAGACCAT 60  
QY 72 CCGACTTTTAATAAATAATCTCCAAATTTAGCCGAATTTGCTTTTCTTTGTATAGACAA 131  
DB 61 CCGACTTTTAATAAATAATCTCCAAATTTAGCCGAATTTGCTTTTCTTTGTATAGACAA 120  
QY 132 TTAGCTCATCAAAAGTAATTTACTTAACATTTTTTTTAGTCTCTTTCTATTGCGACTGCT 191  
DB 121 TTAGCTCATCAAAAGTAATTTACTTAACATTTTTTTTAGTCTCTTTCTATTGCGACTGCT 180  
QY 192 TTGCGCCATGTGAGTTAGTACTATAAGCGCATACCCATGACGAGATTTTAGAAGGTTTA 251  
DB 181 TTGCGCCATGTGAGTTAGTACTATAAGCGCATACCCATGACGAGATTTTAGAAGGTTTA 240  
QY 252 AACTTTAATTTGACCGAAATCCCAAGAGCCCAATTCACGAGGTTTTCAGAGTTGTG 311  
XX  
XX

DB 241 AACTTTAATTTGACCGCAAAATCCAGAGCCCAAAATTCACGAGGGTTTTCAAGAGTTGTTG 300  
QY 312 AGAAGCTTTGAATCAACCTGATTTCTCAATTTGCAATTTAACTACTGTTAAACGGTTTATTTTGG 371  
DB 301 AGAAGCTTTGAATCAACCTGATTTCTCAATTTGCAATTTAACTACTGTTAAACGGTTTATTTTGG 360  
QY 372 TCTGAAGGTTTAAATTTGTTGACAAATTTCCCTAGAGAGCTCAAGAAACATATATCATAGT 431  
DB 361 TCTGAAGGTTTAAATTTGTTGACAAATTTCCCTAGAGAGCTCAAGAAACATATATCATAGT 420  
QY 432 GAGGCTTTTACCGTTAAATTTTGGTGATCTGAGGAGCTTAAAGCAAAATTAATGATTAT 491  
DB 421 GAGGCTTTTACCGTTAAATTTTGGTGATCTGAGGAGCTTAAAGCAAAATTAATGATTAT 480  
QY 492 GTTGAGAAAGGACCCAGGGTAAGATCGTTGACCTAGTTTAAAGAAATTAGATCGTGATACC 551  
DB 481 GTTGAGAAAGGACCCAGGGTAAGATCGTTGACCTAGTTTAAAGAAATTAGATCGTGATACC 540  
QY 552 GTCTTCGCACCTAGTTAACTATATTTTTTCAAGGGTAAGTGGGAAACGCTCTTTCGAGGTT 611  
DB 541 GTCTTCGCACCTAGTTAACTATATTTTTTCAAGGGTAAGTGGGAAACGCTCTTTCGAGGTT 600  
QY 612 AAAGTACTGAAGAGGAGATTTTCATGTTGATCAAGTTTACTACTCTCAAAAGTTCCAATG 671  
DB 601 AAAGTACTGAAGAGGAGATTTTCATGTTGATCAAGTTTACTACTCTCAAAAGTTCCAATG 660  
QY 672 ATGAAAAGACTGGGTATGTTTCAATATTCACATTTGCAAAATTTAAGTTCTTGGGTCTTA 731  
DB 661 ATGAAAAGACTGGGTATGTTTCAATATTCACATTTGCAAAATTTAAGTTCTTGGGTCTTA 720  
QY 732 TTAATGAACATATTTAGTGAACCTACTGCTATTTTTTTTACCAGAGAGGTAAGCTT 791  
DB 721 TTAATGAACATATTTAGTGAACCTACTGCTATTTTTTTTACCAGAGAGGTAAGCTT 780  
QY 792 CAACATTTAGAGAATGAGTTGACTCATGACATTTACTATAATTTTAGAGAACGAGAT 851  
DB 781 CAACATTTAGAGAATGAGTTGACTCATGACATTTACTATAATTTTAGAGAACGAGAT 840  
QY 852 CGTCGTAGCGCTTCTGCAACCTGCCAAAGTTAAGTATCACCGGTACTTACGACTTAA 911  
DB 841 CGTCGTAGCGCTTCTGCAACCTGCCAAAGTTAAGTATCACCGGTACTTACGACTTAA 900  
QY 912 TCTGTTTTAGGCGAGTTAGGTATTTACCAAGTTTCTTAAACGGTCCGATTTGAGTGGT 971  
DB 901 TCTGTTTTAGGCGAGTTAGGTATTTACCAAGTTTCTTAAACGGTCCGATTTGAGTGGT 960  
QY 972 GTTACTGAAGAAGCTCCATTAATAATTTGAGTAAAGCTGTTTCAAAAGCGGTCTTAACTATT 1031  
DB 961 GTTACTGAAGAAGCTCCATTAATAATTTGAGTAAAGCTGTTTCAAAAGCGGTCTTAACTATT 1020  
QY 1032 GATGAAAAGGTTACCGAGCGCGCGCTATGTTCTCGAAGCTATTTCCCAATGAGCAT 1091  
DB 1021 GATGAAAAGGTTACCGAGCGCGCGCTATGTTCTCGAAGCTATTTCCCAATGAGCAT 1080  
QY 1092 CCACCAAGAGTTTAAATTTAAATTAACCATTTCTGTTTCTGATGATCGAGCAGAACACTAAA 1151  
DB 1081 CCACCAAGAGTTTAAATTTAAATTAACCATTTCTGTTTCTGATGATCGAGCAGAACACTAAA 1140  
QY 1152 AGCCCATGTTTATGGGTAAGGTTGTCACCCCACTCAGAAG 1193  
DB 1141 AGCCCATGTTTATGGGTAAGGTTGTCACCCCACTCAGAAG 1182

RESULT 8

AAV41730

ID AAV41730 standard; DNA; 1260 BP.

XX AC AAV41730;

XX AC AAV41730;

DT 20-NOV-1998 (first entry)

XX Codon-optimised Ramy3D signal fused to DNA encoding mature AAT.

XX





XX Nucleotide sequence of the alpha-1-antitrypsin.  
DE Human alpha-1-antitrypsin; ATR-1; antibody; ATR-1 deficiency; ss.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FT CDS 28..1257  
FT /\*tag= a  
FT /product= "alpha-1-antitrypsin"  
XX US5736379-A.  
XX 07-APR-1998.  
XX 07-JUN-1995; 95US-0479545.  
XX 20-MAY-1982; 82US-0380310.  
XX 07-FEB-1984; 84US-0638980.  
XX 03-MAR-1987; 87US-0022543.  
XX 15-DEC-1987; 87US-0133190.  
XX 16-SEP-1988; 88US-0246912.  
XX 22-AUG-1989; 89US-0398288.  
XX 11-MAR-1991; 91US-0666450.  
XX 18-NOV-1992; 92US-0979556.  
XX 02-JUL-1993; 93US-0086442.  
XX 12-DEC-1994; 94US-0361689.  
XX (WASH-) WASHINGTON RES FOUND.  
XX PA Davie EW, Kurachi K, Thirumalachari C, Woo SLC;  
XX WPI; 1998-239214/21.  
XX DR P-PSDB; AAW56709.  
XX PT DNA encoding alpha-1 anti-trypsin - useful for, e.g. producing  
XX recombinant alpha-1 anti-trypsin  
XX Claim 1; Fig 1; 15pp; English.  
XX This is the nucleotide sequence encoding the novel human  
XX alpha-1-antitrypsin (ATR-1) protein. Its products are useful for  
XX producing recombinant ATR-1 polypeptides, which can be used to prepare  
XX antibodies for detecting ATR-1 variants in the blood, as ligands in  
XX assays for ATR-1, and to treat ATR-1 deficiency.  
XX SQ Sequence 1312 BP; 339 A; 368 C; 324 G; 281 T; 0 other;  
Query Match 28.3%; Score 432.2; DB 19; Length 1312;  
Best Local Similarity 60.4%; Pred. No. 1.1e-98;  
Matches 713; Conservative 0; Mismatches 469; Indels 0; Gaps 0;  
QY 12 GAAGACCTCAAGGCGCGCTCAAAAACCGACACAGTCATCAGCAACCAAGCCAT 71  
DB 100 GAGGATCCCGAGGAGATCTGCCAAGACAGATACATCCCATCATGATCAGGATCAC 159  
QY 72 CCGACTTTTAAATAAATTTACTCCAAATTTAGCGAATTTTCTTTTCTTTGTATAGACAA 131  
DB 160 CCAACCTTCACAGATACCCCACTTGGGTGAGTTCGCTTCAGCCATATACGCCAG 219  
QY 132 TTAGCTCATCAAGTAATTTCTACTAATTTTCTTTAGTCCCTGTTCTATTGCCACTGCT 191  
DB 220 CTGGCACACAGTCCCAACAGACCAATATCTTCTTCTCCCGAGTGAGCATCGCTACAGCC 279  
QY 192 TTCCCATGTTGAGTTAGTACTACGCGATACCCGATGACGAGATTTTAGAAGGTTTA 251  
DB 280 TTTTGAATGCTCTCCCTTGGGGACCAAGCTTGACATCAGATGAATCTCTGGAGGCTG 339  
QY 252 AACTTTTAAATTTGACGAAATTTCCAGAAAGCCCAATTTACAGAGGTTTTCAGAGTTGTTG 311  
DB 340 AATTTCAACCTCAGGAGATTCGGAGGCTCAGATCCATGAAAGGCTTCCAGGAACCTCTC 399

QY 312 AGAATCTTGAATCAACCTGATTTCTCAATTTGCAATTAACCTACTGTAACGGTTTATTATTTG 371  
DB 400 CGTACCTTCAACCGACGACAGCAGCTCCAGCTGACACCGGCAATGGCTGTCCTC 459  
QY 372 TCTGAAGGTTTAAATTTGTTGACAAATTTCCCTAGAGAGCTCAAGAACTATATCATAGT 431  
DB 460 AGCGAGGCTGAAGCTAGTGGATAGTTTGGAGGATGTTAAAAAGTTGTACCACTCA 519  
QY 432 GAGGCTTTTACCGTTAAATTTTGGTGTATCTAGGAGAGCTTAAAGCAATTAATGATAT 491  
DB 520 GAAGCTTCTACCTGTCACCTTCGGGACACCGAAGAGGCCAAGAAACAGATCAACGATTAC 579  
QY 492 GTTGAGAAAGGACCCAGGTAAGATCTGTTGACCTAGTTTAAAGAAATTAGATCGTGATACC 551  
DB 580 GTGGAGAAGGGTACTCAAGGAAATTTGGGATTTGGTCAAGAGCTTGACAGACACA 639  
QY 552 GTCTTCGCACTAGTTAACTATATTTTTTCAAGGGTAAGTGGGAAGCTCTTTCAGGTT 611  
DB 640 GTTTTGTCTGTGATTTACATCTTCTTTAAGGCAATGGGAGAGACCTTTGAAGTC 699  
QY 612 AAAGATCTGAAGAGGAAGATTTTCAATGTTGATCAAGTACTACTGTCAAGTTCCAATG 671  
DB 700 AAGCACCGGAGGAGGACTTCCACGTGGACAGGTGACCACTGAGGTGAGGTGCTATG 759  
QY 672 ATGAAAAGACTGGGTATGTTCAATATTTCAATTTCAATTTGCAAAAATTAAGTTCTTGGGTCTTA 731  
DB 760 ATGAAGCGTTTAGGCATGTTTAACTATCCAGCATTTGTAAGAGCTGTCACGTGGGTGCTG 819  
QY 732 TTAATGAAGTATTTAGTAACTGCTACTGCTATTTTTTTTTTACCAGCAAGGTAAGCTTT 791  
DB 820 CTGATGAATACCTGGCAATGCCACCGCATCTTCTCTGCTGATGAGGGAACATA 879  
QY 792 CAACATTTAGAGAAATGAGTTGACTCATGACATTTACTTAAATTTTATAGAGACGAGGAT 851  
DB 880 CAGCACCTGGAAAATGAATCACTCACCAGATATCATCACCAGTTCTCTGGAATAAGAC 939  
QY 852 CGTGTAGCTCTCTCTGCACTGCCAAAGTTAAGTATACCGGTACTTACGACTTAAAA 911  
DB 940 AGAAGGTCTGCCAGCTTACATTTACCCAACTGTCCATTTACTGGAACCTATGATCTGAAG 999  
QY 912 TCTGTTTTAGGCCAGTTAGGTATTTACAAAGTTTTTCTAACGGTGGCGATTTGAGTGT 971  
DB 1000 AGCTCTAGTCACTAAGCTGCGCATCACTAAGCTCTTACGCAATGGGCTGACCTCTCGGG 1059  
QY 972 GTTACTGAAGAGCTCCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1031  
DB 1060 GTCACAGAGGAGGACCCCTGAAGCTCTCCAAAGCCGCTGATAGGCTGTGCTGACCATC 1119  
QY 1032 GATGAAAAGGTACCGAGGCGCGGCTATGTTCTCTGGAAGCTATTTCAATGAGCATTT 1091  
DB 1120 GACGAGAAAGGACTGAAGCTGTGGGCCATGTTTTTAGAGGCCATACCCATGCTATC 1179  
QY 1092 CCACCAGAGTTAAATTAATAAACCAATTCGTTTTCTGATGATCGAGACACACTAAA 1151  
DB 1180 CGCCCGAGGTCAGATTCACAAACCCCTTTGCTCTTTAATGATTGAACAAATATCCAAG 1239  
QY 1152 AGCCATGTTTATGGTAAAGTTGTCAACCCCACTCAGAA 1192  
DB 1240 TCTCCCTCTTCTTATGGGAAAGTGTGTAUCCCAACCAAA 1280

RESULT 11  
AAZ90199  
ID AAZ90199 standard; cdna; 1312 BP.  
XX AAZ90199;  
XX AC  
XX XX  
XX DT 19-MAY-2000 (first entry)  
XX DE Human alpha-1-antitrypsin nucleotide sequence.  
XX KW Alpha-1-antitrypsin; neutrophil elastase inhibitor; human; ss;  
KW chronic obstructive pulmonary emphysema; infantile liver cirrhosis.

XX Homo sapiens.  
 OS US025161-A.  
 PN 15-FEB-2000.  
 PD 20-JAN-1998; 98US-0009581.  
 PF 07-JUN-1995; 95US-0479545.  
 PR 20-MAY-1982; 82US-0380810.  
 PR 07-FEB-1984; 84US-0638980.  
 PR 03-MAR-1987; 87US-0022543.  
 PR 15-DEC-1987; 87US-0133190.  
 PR 16-SEP-1988; 88US-0246912.  
 PR 22-AUG-1989; 89US-0398288.  
 PR 11-MAR-1991; 91US-0666450.  
 PR 18-NOV-1992; 92US-0979556.  
 PR 02-JUL-1993; 93US-0086442.  
 PA (WASH-) WASHINGTON RES FOUND.  
 XX  
 XX Woo SLC, Thirumalachary C, Kurachi K, Davie EW;  
 DR WPI; 2000-181811/16.  
 XX P-PSDB; AAY78890.  
 XX  
 XX preparing alpha1-antitrypsin for inhibiting neutrophil elastase  
 PT involves transfecting host cell with vector comprising  
 PT alpha1-antitrypsin DNA sequence that hybridizes to human  
 XX alpha1-antitrypsin cDNA, or its complement -  
 PS Claim 1; Fig 1; 16pp; English.  
 XX  
 XX This sequence represents the human alpha1-antitrypsin nucleotide  
 CC sequence. Alpha1-antitrypsin is an important protease inhibitor, the  
 CC major function of which is to inhibit neutrophil elastase. Low levels of  
 CC alpha1-antitrypsin in the blood are associated with chronic obstructive  
 CC pulmonary emphysema and infantile liver cirrhosis. A vector comprising a  
 CC mammalian alpha1-antitrypsin DNA sequence that hybridizes to human  
 CC alpha1-antitrypsin cDNA can be introduced into a host cell in a method  
 CC for the production of alpha1-antitrypsin.  
 XX  
 SQ Sequence 1312 BP; 339 A; 368 C; 324 G; 281 T; 0 other;

Query Match 28.3%; Score 432.2; DB 21; Length 1312;  
 Best Local Similarity 60.4%; Pred. No. 1.1e-98;  
 Matches 713; Conservative 0; Mismatches 468; Indels 0; Gaps 0;

QY 12 GAAGACCTCMAGCGGAGCGGCTCAAAAAACCGACACCATCATCAGACCAAGACCAT 71  
 DB 100 GAGGATCCCGAGGAGATGCTGCCAGACACAGATACATCCACCATGATCAGGATCAC 159  
 QY 72 CCGACTTTTAAATAAATTACTCCAAATTTAGCCGAATTTGCTTTTCTTTGTATAGACAA 131  
 DB 160 CCAACCTTCAACAGATACACCCCACTTGGCTGAGTTCGCTTACAGCTTATACCGCCAG 219  
 QY 132 TTAGCTCATCAAAAGTAATTTACTAATATTTTCTAGTCTGCTTTCTTCTGACCTGCT 191  
 DB 220 CTGSCACACAGTCCACACACACCATATCTTCTCTCCCATGTGACATCGCTACAGCC 279  
 QY 192 TTGCGCATTTGAGTTTGTAGTACTAAAGCCGATACCATGACGAGATTTTGTAGAGGTTTA 251  
 DB 280 TTTGCAATGCTCTCCCTGGGAGCAAGGCTGACACTCACGATCAATCTCTGGAGGCGCTG 339  
 QY 252 AACTTTTAAATTTGACGGAATTTCCAGAGCCCAATTTCCAGAGGTTTTCAGAGTTGTTG 311  
 DB 340 AATTCAACTCAGGAGATTCGAGGCTTCAGATCCATGAAGGCTTCAGGAACCTCTC 399  
 QY 312 AGAAGTTTGAATCAACCTGTATCTCAATTGCAATTAACCTACTGTTAAACGGTTTATTTTGG 371  
 DB 400 CGTACCCTCAACAGCCAGACAGCCAGCTCCAGCTGACCCAGCGGCAATGGCTGTTCCTC 459

QY 372 TCTGAAGGTTTAAAAATTGGTTGCAAAATTTCTAGAACGCTCAAGAACTATATCATAGT 431  
 DB 460 AGCAGGGGCTGAAGCTAGTGGATAAGTTTTTGGAGGATGTTAAAAAGTTGTACCACTCA 519  
 QY 432 GAGGCTTTTACCGTTAAATTTTGGTGATCTAGGAGAGCTAAAAAGCAAAATTAATGATTAT 491  
 DB 520 GAAGCCTTCACTGTCAAACTTCGGGGACACGAAGAGGCCAAGAACAGATCAACGATTAC 579  
 QY 492 GTTGAGAAAGGACCCAGGGTAAAGATCGTTGACCTAGTTAAAGAAATTAGATCTGATACC 551  
 DB 580 GTGGAGAGGGTACTCAAGGGAATAATTTGGTTCAGGAGCTTGACAGAGACACA 639  
 QY 552 GTCTTCCACTAGTTAACTATATTTTCAAGGGTAAAGTGGGAAGCTCTTTTCGAGGTT 611  
 DB 640 GTTTTGTCTGTGGTGAATTAATCATCTCTTTTAAAGGCAATGGCAGAGACCTTTGAAGTC 699  
 QY 612 AAGATACCTCAAGAGGAGATTTTTCATGTGTGATCAAGTTACTACTGTCAAGTTCCAATG 671  
 DB 700 AAGACACCCAGGAAGAGGACTTCCACGTGGACAGGTGACCACTGAAAGTGCCTATG 759  
 QY 672 ATGAAAGACTGGGTATGTTCAATATTTCAACATTTGCAAAAAATTAAGTTCTTGGGCTTA 731  
 DB 760 ATGAAGGCTTTAGGCATGTTTAACATCCAGCATTTGAAGNAGCTGTCCAGCTGGGTGCTG 819  
 QY 732 TTAATGAAGTATTTAGGTAAAGCTACTGCTATTTTTTTTTTACCAGACGAAGTAAAGCTT 791  
 DB 820 CTGATGAAATACCTGGGCAATGCCCGCATCTTCTCTCTGCTGCTGATGAGGGAACATA 879  
 QY 792 CAACATTTAGAGAAATGAGTTGACTCATGACATTAATTAATTTTTTAGAGNACGAGGAT 851  
 DB 880 CAGCAGCTGGAATGAATCACTCCACGATATCATCACCAGTTTCTGTGAAAATGAAGAC 939  
 QY 852 CGTGTAGCGCTTCTCTGCACCTGCCAAAGTTAAAGTATCACCGGTACTTACGACTTAAAA 911  
 DB 940 AGAAGGCTGCCAGCTTACATTTTACCCAAACTGTCCATTTACTGGAACCTATGATCTGAAG 999  
 QY 912 TCTGTTTTAGGCCAGTTAGTATTACCAAGTTTTTTTCTAACGGTGGCCGATTTGAGTGTG 971  
 DB 1000 AGCGTCTAGGTCAACTGGGCATCACTAAGAGTCTTTCAGCAATGGGGCTGACCTCTCCGG 1059  
 QY 972 GTTACTGAAGAGCTCCATTAATAATTTAGTAAAGCTGTTTCAACAAAGCCGCTCTTAATATT 1031  
 DB 1060 GTCACAGAGGAGGACCCCTCGAAGCTCTCCAAGGCCGTGCATAGGCTGTGCTGACCATC 1119  
 QY 1032 GATGAAAGGGTACCGAGCGCGCGGCTATGTTCTCGAAGCTATTCCAAATGAGCAAT 1091  
 DB 1120 GACGAGAAAGGAGCTGAAGCTGCTGGGGCATGTTTTTATAGAGGCCATACCCATGCTATC 1179  
 QY 1092 CCACCAAGAGTTAAATTTAAATTAACCATTCGTTTTTCTGATGATCGAGCAGAACACTAAA 1151  
 DB 1180 CGCCCCGAGGTCAAGTTCAACAAACCCCTTTGTCTTTAATGATTGAACAAAAATACCAAG 1239  
 QY 1152 AGCCCATTTTATGGTAAAGTTGTCAACCCCACTCGAA 1192  
 DB 1240 TCTCCCTCTTCATGGGAAAAGTGGTGAATCCACCCCAAAA 1280

RESULT 12  
 AAS45052  
 ID AAS45052 standard; cDNA; 1367 BP.  
 XX  
 AC AAS45052;  
 XX  
 XX  
 DT 18-DEC-2001 (first entry)  
 XX  
 DE cDNA encoding novel human secretory protein, Seq ID No 133.  
 XX Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;  
 KW ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;  
 KW transgenic animal; Alzheimer's disease; Parkinson's disease; burn;  
 KW amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;  
 KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;  
 KW gut protection; lung; liver fibrosis; immune deficiency; infection;

severe combined immunodeficiency; SCID; autoimmune disorder; allergy; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma; fertility; analgesic; pain; antigen; ss.

OS Homo sapiens.

XX WO200166689-A2.

XX 13-SEP-2001.

XX 05-MAR-2001; 2001WO-US04942.

XX 07-MAR-2000; 2000US-0519705.

XX 19-MAY-2000; 2000US-0574454.

XX 17-JUN-2000; 2000US-0596193.

XX 14-JUL-2000; 2000US-0616847.

XX 19-SEP-2000; 2000US-0665363.

XX 20-OCT-2000; 2000US-0693267.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P; Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J; WPI: 2001-589934/66.

XX P-PSDB; AAU28152.

XX Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis and treatment of cancer, neurological, inflammatory, and autoimmune disorders - Claim 1; SEQ ID No 133; 107pp; English.

XX The invention relates to novel isolated human secreted polypeptides (I) and polynucleotides (II). (I) and (II) are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's disease, ischaemia-reperfusion injury, shock, sepsis, immune responses, and is involved in increasing haematopoiesis, stem cell survival, bone growth and remodeling. (I), (II) and modulators of (II) are useful for prophylaxis or treatment of one or more cancers. (II) is also useful for creating transgenic animals useful for studying the in vivo activities of the polypeptide as well as for studying modulators of the polypeptides. (I) induces the proliferation of neural cells and regeneration of nerve and brain tissue and is useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's disease, Huntington's disease, and amyotrophic lateral sclerosis. In addition, (I) is involved in chemotactic or chemokinetic activity, regulation of haematopoiesis and is useful for treating myeloid or lymphoid cell disorders, platelet disorders such as thrombocytopenia and for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, and in tissue repair, healing of burns, incisions, ulcers, for treating osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease. Furthermore, (I) is also useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic reactions and conditions, such as asthma or other respiratory problems. In addition, (I) affects biorhythms or circadian cycles of rhythms, fertility, metabolism, catabolism, anabolism, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides analgesic effects or other pain reducing effects, immunoglobulin like activity and can act as an antigen in a vaccine composition to raise an immune response. AAS44920-AAS45295 represent novel human secreted protein coding sequences of the invention.

XX Sequence 1367 BP; 357 A; 392 C; 323 G; 295 T; 0 other;

Query Match 28.1%; Score 429.2; DB 22; Length 1367;  
Best Local Similarity 60.7%; Pred. No. 6.6e-98;  
Matches 718; Conservative 0; Mismatches 463; Indels 1; Gaps 1;

QY 12 GAAGACCCCTCAAGCGCAGCGCGCTCAAAAACCGCAGCAGTCATCACGACCAAGCAAT 71  
DB 105 GAGATCCCGCAGGAGATGCTGCCAGAGAGACATACATCCACCATCAGGATCAC 164  
QY 72 CCGACTTTTAATAAATTTACTCCAAATTTAGCGGAATTTGCTTTTCTTTGATAGACAA 131  
DB 165 CCAACCTTCAACAAGATCAACCCCAACCTGGCTGAGTTCCGCTTACGCTATACCCCGAG 224  
QY 132 TTAGCTCATCAAGATTAATTTCTACTTAACATTTTCTTTAGTCTCTTTTCTTCTTCT 191  
DB 225 CTGGCACACCGATCCACAGCAGCAATATCTTCTTCTCCCGAGTGAGCATCGCTACAGCC 284  
QY 192 TTGCGCATGTTGAGTTTAGGTACTAAAGCGGATACCCATCAGCAGAGATTTTGAAGTTTA 251  
DB 285 TTTGCAATGCTCTCCCTGGGGACCAAGGCTGACACTCAGATGAAATCTCTGGAGGCGCTG 344  
QY 252 AACTTTAATTTGACCGGAATTCACAGAGCCCAATTCAGAGGGTTTCAAGAGTTGTTG 311  
DB 345 AATTTCAACCTCAGGAGATTCGGAGGCTCAGATCCATGAAGGCTTCAGGAACCTCCTC 404  
QY 312 AGAATTTGAATCAACCTGATTTCTCAATTTGCAATTAAGTACTTCTTAACTTCTTAACTT 371  
DB 405 CGTACCTCTCAACCGCAGCAGCAGCAGCTCCAGTGCACCGCAATGGCTTCTTCTC 464  
QY 372 TCTGAAGGTTTAAATTTGGTTGACAAATTCCTAGAGAGCTCAAGAACTATATCATAGT 431  
DB 465 AGCGAGGCGCTGAGCTAGTGGATAGTTTGGAGGATGTTAAAGTTTGTACCACTCA 524  
QY 432 GAGCGTTTTCACGTTAAATTTTGGTGAT-ACTGAGGAAGCTTAAAGCAAAATTAATGATTA 490  
DB 525 GAACCTTCACTGTCACCTTCGGGGATCACCGAAGGCGCAAGAACAGATCAACGATTA 584  
QY 491 TGTGAGAAAGGCGCAGGGAAGATCGTTGACCTAGTTTAAAGATTTAGATCGTGATAC 550  
DB 585 CGTGAGAAAGGCTACTCAAGGGAATTTGGTATTTGTCAGAGGAGTTTCAAGAGACAC 644  
QY 551 CGTCTTTCGCACTAGTTTAACTATATTTTCAAGGGAAGTGGGAAGCTGCTTTCGAGGT 610  
DB 645 AGTTTTCGCTGCTGTTGATATACATCTTCTTAAAGGCAATGGGAGAGACTTTTGAAGT 704  
QY 611 TAAAGATCTCAAGAGGAAGATTTTCATGTTGATCAAGTTTACTTCTCTCAAGTTCCAAT 670  
DB 705 CAAGACACCGCAGGAGGAGGACTTCCAGTGGACCGAGTGCACCGCTGAAGGTCCCTAT 764  
QY 671 GATGAAAGACTGGGTATGTTCAATATTCACATTCAGAAATTAAGTTCTTGGGCTT 730  
DB 765 GATGAAGGCTTTAGGCAATGTTTAACTCCAGCATCTGAAGAGCTGTCCAGCTGGGTACT 824  
QY 731 ATTAATGAAGTATTTAGTAAAGCTACTGCTATTTTCTTTTACCAGAGGAGTAAGCT 790  
DB 825 GCTAATGAATACCTGGSCAATGCCACCGCATCTTCTTCTTCTGATGAGGGAACCT 884  
QY 791 TCACATTTAGAGAAATGAGTTGACTCATGACATTTACTTAATTTTAGAGAACGAGGA 850  
DB 885 ACAGACCTGGAATTAAGTCAACCCAGATATCATCAACCAAGTTTCTTGGAAATGAGA 944  
QY 851 TCGTGTAGCGCTTCTCTGCACTTCCCAAGTTAAGTATACCGGTACTTACGACTTAAA 910  
DB 945 CAGAAGTCTGCCAGCTTACATTTACCAAACTGTCCATTTACTGGAACCTATGCTGAA 1004  
QY 911 ATCTCTTTTAGGCCAGTTAGGTATTTACAAAGTTTCTTAAAGTCCCGATTTGAGTGG 970  
DB 1005 GAGCGTCTGGGTCAACTGGGCTACCTTAAGGTCTTTCAGCAATGGGCTGACCTCTCGG 1064  
QY 971 TGTGTTGAAGAGCTCCATTAATTAAGTAAAGCTGTTCCAAAGCGGCTTCTTAACTAT 1030  
DB 1065 GGTACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1124  
QY 1031 TGATGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1090  
DB 1125 CGACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1184  
QY 1091 TCCACCAGAAAGTAAATTTAATAAACCATTCGTTTTTCTGTGATCGAGCAGACACTAA 1150

Db 1185 CCCCCAGAGGTCAGATTCACAAACCCCTTGTCTCTTAATGATGACAAATACCAA 1244  
QY 1151 AAGCCCATGTTATGGGTAAGGTTGTCACCCCAACTCAGAA 1192  
Db 1245 GTCTCCCTCTTTCATGGGAAAGTGGTGAATCCCAACCAAAA 1286

## RESULT 13

AAV41726

ID AAV41726 standard; DNA; 1185 BP.

XX AAV41726;

AC XX

XX 20-NOV-1998 (first entry)

DT XX

XX Native coding sequence of mature alpha1-antitrypsin (AAT).

DE XX

XX Protein expression; monocotyledon plant cell;

KW glycosylated alpha 1-antitrypsin; AAT; glycosylated antithrombin III;

KW ATIII; human serum albumin; HSA; subtilisin BPN'; treatment; emphysema;

KW antithrombotic; blood replacement; ss.

XX Homo sapiens.

OS XX

XX W09836085-A1.

PN XX

XX 20-AUG-1998.

PD XX

XX 13-FEB-1998; 98WO-US03068.

XX PF

XX 13-FEB-1997; 97US-0038170.

XX PR

XX 13-FEB-1997; 97US-0037991.

XX PR

XX 13-FEB-1997; 97US-0038168.

XX PR

XX 13-FEB-1997; 97US-0038169.

XX XX

PA (PHYT-) APPLIED PHYTOLOGICS INC.

XX Rodriguez RL, Sutcliffe TD;

XX WPI; 1998-467179/40.

XX DR P-PSDB; AAW59839.

XX XX

XX Expressing mature, glycosylated proteins in monocotyledonous plant

XX cells - from chimeric gene including signal peptide sequence,

XX specifically therapeutic agents and industrial enzymes

XX PS Disclosure; Page 29; 53pp; English.

XX XX

XX The present sequence represents the native coding sequence of mature

XX alpha1-antitrypsin (AAT). The protein is used to exemplify the

XX invention. The specification describes a method for producing mature

XX heterologous protein in monocotyledonous plant cells. The method

XX comprises transforming the cells with a chimeric gene comprising a

XX monocotyledon transcription regulator, inducible either during seed

XX maturation or by adding/removing a small molecule, DNA encoding the

XX heterologous protein, and DNA encoding a signal peptide, with

XX the signal peptide causing secretion of the protein from the cell.

XX Proteins expressed in this manner include mature glycosylated alpha

XX 1-antitrypsin (AAT) with a glycosylation pattern that significantly

XX increases its serum half-life, mature glycosylated antithrombin III

XX (AATIII), mature human serum albumin (HSA) having the native folding

XX pattern as shown by bilirubin-binding characteristics, or mature active

XX subtilisin BPN'. These proteins are useful therapeutically (e.g. AAT for

XX treating emphysema, AATIII as antithrombotic and HSA as blood replacement)

XX or as industrial enzymes (BPN' is used in detergents).

XX XX

XX Sequence 1185 BP; 328 A; 324 C; 283 G; 250 T; 0 other;

XX XX

XX Query Match 28.1%; Score 429; DB 19; Length 1185;

XX Best Local Similarity 60.2%; Pred. No. 7.1e-98;

XX Matches 711; Conservative 0; Mismatches 470; Indels 0; Gaps 0;

XX XX

QY 12 GAAGACCTCAAGCGGAGCGCGGTCAAAAAACCGACACACAGTCAATCAGACACCAAGACCAT 71  
Db 1 GAGGATCCCGAGGAGATGCTGCGCCAGAGACAGATACATCCCAACCATGATCAGGATCAC 60  
QY 72 CCGACTTTTAAATAAATTTACTCCAAATTTAGCCGAATTTGCTTTTCTTTCTTTGATAGACAA 131  
Db 61 CCAACCTTCAACAGATCACCCCAACCTGGCTGAGTTCCGCTTCAGCCTATACCGCCAG 120  
QY 132 TTAGCTCATCAAAAGTAATTTCTACTAACAATTTTTTTTATAGTCTCTGTTCTATTTGCCACTGT 191  
Db 121 CTGGCACACCAAGTCCCAACAGACCAATATCTTCTTCCCCAGTGAGCATCGCTACAGCC 180  
QY 192 TTGCCATGTTGAGTTTAGGTACTAAAGCCGATACCCATGACAGATTTTAGAAGGTTTA 251  
Db 181 TTTGCAATGCTCTCCCTGGGAGCCAAAGGCTGACATCAGATGAAATCTCTGGAGGCCCTG 240  
QY 252 AACTTTAATTTGACCGAAATCCAGAGGCCAAATTCACGAGGGTTTTCAGAGTGTGTTG 311  
Db 241 AATTTCAACCTCAGGAGATTCGGAGGCTCAGATCCATGAGGCTTCCAGGAACCTC 300  
QY 312 AGAATTTGAATCAACCTGATTTCTCAATTGCAATTTAACTACTGTAACGGTTTATTTTGG 371  
Db 301 CGTACCCTCAACAGCCAGACAGCAGCTCCAGCTGACCAACCGCAATGCGCTGTTCCCTC 360  
QY 372 TCTGAAGTTTAAATTTGTTGATGACAAATTTCTAGAGACGTCAGAAATATATCATAGT 431  
Db 361 AGCGAGGGCTGAGGCTAGTGGATAAGTTTGGAGGATGTTTAAAGTTGTACCACTCA 420  
QY 432 GAGCTTTTACCGTTAATTTTGGTGATGAGGAGCTAAGGCTAAGGCTAAGGCTAATAT 491  
Db 421 GAGCCTTCACTGTCAACTTCGGGGACCCGAGAGGCCAAGAAACAGATCAACGATTA 480  
QY 492 GTTGAGAAAGGCCACCCAGGTAAGATCGTTGACCTAGTTTAAAGAAATTAGATCGTATACC 551  
Db 481 GTGGAGAAGGGTACTCAAGGGGAAATTTGTGATTTGGTCAAGGAGCTTGACAGACACA 540  
QY 552 GTCTTCCACTAGTTTAACTATATTTTTTCAAGGGTAAGTGGGAAGCTGCTTTTCGAGGTT 611  
Db 541 GTTTTCTCTGTTGATTAATTAATTAATTAAGGCTAAGGCTGAGGAGAGCCCTTTGAAGTC 600  
QY 612 AAAGATACTCAAGAGGAAGATTTTCAATGTTGATCAAGTTACTACTGTCAGAGTTCCAATG 671  
Db 601 AAGGACACCGAGAGAGGAGCTTCCAGCTGGGACCGAGTGCACCGCTGAAGGTGCGCTATG 660  
QY 672 ATGAAAGACTGGGTATGTTTCAATATTCACATTTGCAAAATTTAAAGTTCTTGGGTCTTA 731  
Db 661 ATGAAGCGTTTAGGCATGTTTAACTCCAGCACTGTAAGAAGCTGTCAGCTGGGTGCTG 720  
QY 732 TTAATGAAGTATTTAGTTAAGCTACTGCTATTTTTTTTTTACCAGACGAGTAAGCTTT 791  
Db 721 CTGATGAAATTAATGAGGCAATGCGCCGCTATCTTCTGCTGCTGATGAGGGGAACATA 780  
QY 792 CAACATTTAGAGAAATGAGTTGACTCATGATTAATTAATTAATTAATTAATTAATTAAT 851  
Db 781 CAGCAGCTGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 840  
QY 852 CGTCGTAGCGCTTCTCTGCACTGCGCAAGTAAAGTATCACCAGGTACTTACGACTTTAAA 911  
Db 841 AGAAGGTCTGCCAGCTTACATTTTACCAAACTGCTCCATTTACGAACTATGATCTGAAG 900  
QY 912 TCTGTTTTAGGCCAGTTAGTATTTACCAAAAGTTTTTCTAACGGTCCGATTTGAGTGTG 971  
Db 901 AGCGTCTCGGTGCACTGGGCTACATAAGGCTCTTCCAGCAATGGGCTGACCTCTCCGGG 960  
QY 972 GTTACTGAAGAAGCTCCATTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1031  
Db 961 GTCACAGAGGAGGACCCCTGAGGCTCTCCAGGCGCTGCATTAAGGCTGCTGACCATC 1020  
QY 1032 GATGAAAGGGTACCAGGCGCGCGCTATGTTCTCGGAAGCTATTTCCTGAGCAATTTAGAGCA 1091  
Db 1021 GAGGAGAAAGGGGACTCAAGCTGCTGGGGCATGTTTTTTAGAGGCCATACCCATGCTATC 1080  
QY 1092 CCACCAGAGTTAAATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1151

Db 1081 CCCCCGAGTCAAGTTCAACAAACCCCTTTGTTCTTAAATGATTGAACAAATAACCAAG 1140  
Qy 1152 AGCCCATGTTTATGGTGAAGTTGTCAACCCCAACTCAGAA 1192  
Db 1141 TCTCCCTCTTCAATGGGAAAAGTGGTGAATCCACCCAAAA 1181

## RESULT 14

AAQ31403

ID AAQ31403 standard; DNA; 1352 BP.

XX AC

XX AC

XX AAQ31403;

DT 23-MAR-1993 (first entry)

XX Human alpha-1 antitrypsin.

DE Human alpha-1 antitrypsin.

XX Plasmid; pCMV4; liposome; antiprotease; lung; emphysema;

KW adult respiratory distress syndrome; ARDS; ss.

XX Homo sapiens.

OS W09219730-A.

XX 12-NOV-1992.

XX 27-MAR-1992; 92WO-US02465.

XX 24-APR-1991; 91US-0690283.

PR (UYVA-) UNIV VANDERBILT.

XX Brigham K, Canonico A, Conary J, Meyrick B;

PI WPI; 1992-398857/48.

XX Human alpha-1 anti-trypsin contg. plasmid - for treatment of

PT anti-protease deficiency in emphysema and other lung diseases

PS Disclosure; Fig 6a-6b; 32pp; English.

XX A plasmid consisting of a pCMV4 expression vector including a coding

CC sequence of human alpha-1 antitrypsin may be incorporated into

CC liposomes capable of targeting specific tissue. The plasmid is then

CC capable of expression of the gene extrachromosomally in the cells of

CC the target tissue and is unincorporable into the chromosome of the

CC cells of the target tissue. Thus, the liposome including the

CC plasmid can be used in a method for treating a deficiency of the

CC gene product in cells of the target tissue.

CC The specific use of the human alpha-1 antitrypsin is significant as

CC this antiprotease is important in protecting the lungs against

CC emphysema. The adult respiratory distress syndrome (ARDS) is thought

CC to involve a relative deficiency of antiprotease activity.

CC Therefore, the delivery of a functioning alpha-1 antiprotease

CC gene to the lungs can be therapeutic in many human conditions

CC characterised by injury of the lungs.

XX Sequence 1352 BP; 349 A; 386 C; 325 G; 292 T; 0 other;

SQ

Query Match 28.1%; Score 429; DB 13; Length 1352;  
Best Local Similarity 60.2%; Pred. No. 7.4e-98;  
Matches 711; Conservative 0; Mismatches 470; Indels 0; Gaps 0;

Qy 12 GAAGACCCTCAAGGGAGCGCGCTCAAAAAACCGACACAGTCATCAGCAACCAAGACCAT 71  
Db 92 GAGGATCCCCAGGAGATGCTGCCAGAAAGACAGATACATCCACCATGATCAGATCAC 151  
Qy 72 CGGACTTTTAAATAAATTAATCTCAAAATTTAGCCGAATTTGCTTTCTTTATAGACAA 131  
Db 152 CCAACCTTCAACAGATACACCCCAACCTGGCTGAGTTCGGCTTCAGCCTATACGGCCAG 211  
Qy 132 TTAGCTCATCAAGTAANTCTACTAACATTTTTTTTAGTCTCTGTTCTATTGGCCACTGCT 191

RESULT 15





Mon Dec 9 12:50:32 2002

672	QY	ATGAAAGACTGGGTATGTTCAATATTCAACATTCGAAAATAATTAAAGTTCCTGGGTCTTA	731
752	Db	ATGAAAGGTTTTAGGCATGTTTTAAACATCCAGCACTGAAGAAGCTGTCCAGCTGGGTGCTG	811
732	QY	TTAATGAAGTATTTAGTGAACGCTACTGTATTATTTTTTTTACCAGACGAAGGTAAAGCTT	791
812	Db	CTGATGAATACCTTGGCAATGCCACGCCATCTTCTCTGCTGATGAGGGGAAACTA	871
792	QY	CAACATTTAGAAATAGTATTGACTCATGACATTAATTAATTAATTTTAGAGAACACGAGAT	851
872	Db	CAGCACTTGGAAATAGAACTACCCAGATATCATCACAAGTTCTTGAAAATGGAAC	931
852	QY	CGTCGTAGCGCTTCTCTGCACCTGCCAAAGTTAAGTATCACCGTACTTACGACTTAAA	911
932	Db	AGAAGTCTGCCAGCTTACATTTACCCAAACTGTCCATTACTTGGAACTTATGATCTGAAG	991
912	QY	TCGTGTTTTAGGCCAGTATTAGGTATTACAAAGTTTTTTTCTAACGGTCCCATTTGAGTGGT	971
992	Db	AGCGTCCTGGGTCAACTGGGCATCACTAAGGTCTTCAGCAATGGGCTGACCTCTCCGGG	1051
972	QY	GTTACTGAAGAAGCTCCATTAAAAATTGAGTAAAGCTGTTTCAAAAAGCCGTCTTAACATT	1031
1052	Db	GTCACAGAGGAGGCACCCCTGAAGCTCTCCAAGCCGTGCATAAAGCTGTGTGTGACCATC	1111
1032	QY	GATGAAAAGGTTACGAGGCCCGCGGCTATGTTCTTGGAACTATTCCAATGACCAT	1091
1112	Db	GACGAGAAGGACTTGAAGCTGCTTGGGGCCATGTTTTTAGAGCCCATACCATGTCTATC	1171
1092	QY	CCACCAGAAGTTAAATTTAATAAACCAATTCGTTTTCTTGATGATCGAGCAGACACATAA	1151
1172	Db	CCCCCGAGGTCAGTTCACAAACCCCTTGCTCTCTTAATGATTGAACAAAATACCAAG	1231
1152	QY	AGCCCATTTGTTTATGGGTAAAGTTGTCAACCCCACTCAGAA	1192
1232	Db	TCCTCCCTCTTCATGGGAAAAGTGGTGAATCCCAACCCAAAA	1272

Search completed: December 6, 2002, 23:44:55  
Job time : 238.5 secs